```
============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2010; month=7; day=27; hr=11; min=15; sec=3; ms=141; ]
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Reviewer Comments:
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 15                 20                  25                  30


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ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
           50                  55                  60


tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
       65                  70                  75


gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
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Please remove the blank line between the above row of codons and their
respective amino acids; the amino acids should appear directly below
their their codons.
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<210> 15
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
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<223> k = g or t.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15   20   25   30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
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                50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
            65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291
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        80   85   90

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Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
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gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
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                115   120   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
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                130   135   140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
            145   150   155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160   165   170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175   180   185   190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att   627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile

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            225                    230                 235

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat   771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                    245                250

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat   819
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aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta   963
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aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag   1107
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415                 420                 425                 430

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            450                 455                 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg    1443
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atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
        480                 485                 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc    1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                 500                 505                 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                       1576
Asn Asp Gly Ser Val Ile
                515
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1) Please remove the blank line between the above row of codons and
their amino acids; 2) the above <220>-<223> section describing "k" at

location 1578 is incorrect; the sequence only has 1576 nucleotides.
Same errors in Sequences 17, 19, 21, 23, 25, 27, 29, 31, 35, 37, 39 and
41.

<210> 33
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
     heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

<400> 33
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac   51
          Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
           1   5   10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta   99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt   147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
                   35   40   45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct   195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
              50   55   60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat   243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
            65   70   75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga   291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
         80   85   90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct   339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
  95   100   105   110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc   387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
              115   120   125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act   435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
              130   135   140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac   483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
         145   150   155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa   531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
    160   165   170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt   579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
175   180   185   190

```
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att    627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
                195                 200                 205


gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt    675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
                210                 215                 220


gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct    723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala
            225                 230                 235


cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat    771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp
        240                 245                 250


cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat    819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp
255                 260                 265                 270


ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat    867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp
                275                 280                 285


gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc    915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe
                290                 295                 300


aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta    963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu
            305                 310                 315


cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt    1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser
        320                 325                 330


gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc    1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
335                 340                 345                 350


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```
                    355                  360                      365

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Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
              370                  375                  380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc   1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
          385                  390                  395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att   1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
      400                  405                  410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg   1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                  420                  425                  430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta   1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                  435                  440                  445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata   1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
              450                  455                  460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg   1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
          465                  470                  475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg   1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
      480                  485                  490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc   1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                  500                  505                  510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg                      1576
Asn Asp Gly Ser Val Ile
              515
```

Two errors above: 1) the <220>-<223> section describing the "y" at
location 1008 is errored: "g" is at locadtion 1008; 2) the <220>-<223>
section describing the "k" at location 1578 is errored: there are only
1576 nucleotides above.

****

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                    Validated By CRFValidator v 1.0.3

     Application No:                                    Version No:
                            10569000                                  2.0


                       Input Set:



                       Output Set:



                        Started:   2010-07-22 16:44:17.022
                       Finished:   2010-07-22 16:44:19.919
                       Elapsed:    0 hr(s) 0 min(s) 2 sec(s) 897 ms
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       No. of SeqIDs Defined:      42
          Actual SeqID Count:      42

  Error code      Error Description

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  E   336         Empty lines found between the proteins and the dna

  E   336         Empty lines found between the proteins and the dna

  E   336         Empty lines found between the proteins and the dna

  E   336         Empty lines found between the proteins and the dna

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              Output Set:


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              Finished:    2010-07-22 16:44:19.919
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        Total Warnings:    0
          Total Errors:    112
  No. of SeqIDs Defined:   42
      Actual SeqID Count:  42

Error code     Error Description

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SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
       Hannah, L. Curtis
       Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<140> 10569000
<141> 2010-07-22

<150> US 60/496,188
<151> 2003-08-18

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    50   55   60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
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Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85   90   95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100   105   110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
        115   120   125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
    130   135   140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
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                165   170   175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
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Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
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            340   345   350

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Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
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        450   455   460

Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
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aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac   360

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atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt   540

caggcacaca gagaaacaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa   600

cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct   660

gagaaaccga aaggagagca gttgaaagca atgatggttg acaccaccat acttggcctt   720

gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc   780

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aagccaatac cagatttcag cttctatgac cgttttgctc caatttatac acaacctcga   1020

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gaagtggtca tcatagagga cagtttacta atgggtgcgg actactatga gacagaagct   1200

gataaaaaac tccttgccga aaaaggtggc attcctattg gtattgggaa aaattcatgc   1260

atcaggagaa caatcattga caagaatgct cgaattggag acaatgttaa gatactcaat   1320

gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcatcaa aggtggaatt   1380

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<212> PRT
<213> zea mays

<400> 4

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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20                  25                  30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
        35                  40                  45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
    50                  55                  60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65                  70                  75                  80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
                85                  90                  95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
            100                 105                 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
        115                 120                 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
    130                 135                 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145                 150                 155                 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
                165                 170                 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
            180                 185                 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
        195                 200                 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
    210                 215                 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225                 230                 235                 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
                245                 250                 255
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Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
          260                 265                 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
          275                 280                 285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
    290                 295                 300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys
305                 310                 315                 320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
              325                 330                 335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val
              340                 345                 350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile
          355                 360                 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile
    370                 375                 380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala
385                 390                 395                 400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
              405                 410                 415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile
              420                 425                 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala
          435                 440                 445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile
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Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465                 470                 475


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<212>  DNA
<213>  zea mays


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caagctcatg atagtgttct tggaatcatt ctgggaggtg gtgctgggac tagattgtac     180

cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt     240
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tttaactctg cttccctcaa ccgtcacctc tcaagagcct acgggagcaa cattggaggg      360

tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccaga taatccaaac      420

tggtttcagg gtactgcaga tgctgtaagg cagtacttgt ggttgtttga ggagcataat      480

gtgatggaat ttctaattct tgctggcgat cacctgtacc ggatggacta tgaaaagttc      540

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aaacgtgcaa ctgcatttgg cctcatgaaa attgatgaag aagggaggat cattgagttt      660

gctgagaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc      720

cttgatgacg tgagggcaaa ggaaatgcct tatattgcta gcatgggtat ctatgttttc      780

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ggttactggg aagatatcgg taccattgcg gcattttata atgcaaactt gggaataacc      960

aagaagccaa taccagattt cagcttctat gaccgttttg ctccaattta tacacaacct      1020

cgacacctgc caccttcaaa ggttcttgat gctgatgtga cagacagtgt tattggtgaa      1080

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Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
            20                  25                  30

Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
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            35                    40                       45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
        50                    55                    60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65                    70                    75                    80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
                85                    90                    95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
              100                   105                   110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
            115                   120                   125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
        130                   135                   140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
145                   150                   155                   160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
              165                   170                   175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
            180                   185                   190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
          195                   200                   205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
        210                   215                   220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
225                   230                   235                   240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
              245                   250                   255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
              260                   265                   270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
            275                   280                   285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
        290                   295                   300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
305                   310                   315                   320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
              325                   330                   335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
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          340                  345                  350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
         355                  360                  365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
      370                  375                  380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385                  390                  395                  400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
               405                  410                  415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
            420
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